

1 GCTGTGGAA CCTCTCAG CGACGAAC CAGCCAAAG TTTCTGATAG ATTTTGTGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC
 CGACACCCCTT GGAGAGGTGC GCGTGCTTGA GTCTGCTTGA GTCTGCTTGA GTCTGCTTGA GTCTGCTTGA GTCTGCTTGA GTCTGCTTGA GTCTGCTTGA
 101 CATTAGGAA CTCTGGGAC AGAGGCCCC GCGCGCTGA TGGCCGAGG AGGTGGGAC CCAGGACCA GAGCGGCGT GGAACCATTA CCATGGCCCG
 GCAATCCCTT GAGACCCCTG TCTCGCGGG TCTCGCGGG CCGCGGACT ACCGGCTCG TCCACGCTG GGTCTGGGT CCTTGGTAT GGTACCGGGC
 1 MetalArg
 201 GATCCCCAG ACCCTAAAGT TCGTCTCGT TCGTCTCGT CATCTCGG GTCCTGCTG CAGTCTGAC TTTACTCTGCC ACCACTGCC GGCAGGAGGA AGTTCCCCAG
 CTAGGGGTTT TGGGATTTCA AGCAGCAGCA GTAGCAGCG CAGGACGAG GTACGATCG AATGAGACGG TGGTGACGG CCGTCTCTCT TCAAGGGGTC
 4 IleProLys ThrLeuLysP heValValva lIleValAla ValLeuLeup roValLeuAl aTyrSerAla ThrThrAlaA rgGlnGluG1 uValProGln
 301 CAGACAGTG CCCACAGCA ACAGAGGCAC AGCTTCAAG GGGAGGAGT TCCAGCAGGA TCTCATAGAT CAGAACATAT TGGAGCCCTGT AACCCGTGCA
 GTCTGTACC GGGGTGCTGT TGTCTCCGT TCGAAGTTCC CCTCTCTCAC AGGTCTCTCT AGAGTATCTA GTCTTGTATG ACCTCGGACA TTGGGCACGT
 37 GlnThrVala laProGlnG1 nGlnArgHis SerPheLysG lyGluGluCy sProAlaGly SerHisArgS erGluHisTh rGlyAlaCyS AsnProCyStTh
 401 CAGAGGGTGT GGAATTACACC AACGCTTCCA ACAATGAACC TTTCTGCTTC CCATGTACAG TTTGTAAATC AGATCAAAAA CATAAAAGTT CCTGCACCAT
 GTCTCCCA CA CTTAATGTGG TTGCGAAGGT TGTACTTGG AAGAACGAAG GTACATATGC AAACATTTAG TCTAGTTTTT GTATTTTCAA GGACGTGTA
 71 GluGlyVa lAspTyrThr AsnAlaSerA snAsnGluPr oSerCysPhe ProCysThrV alCysLysSe rAspGlnLys HisLysSerS rCysThrMet
 501 GACCAGAGAC ACAGTGTGC AGTGTAAAGA AGGCACCTTC CGGAATGAAA ACTCCCCAGA GATGTGCCGG AAGTGTAGCA GGTGCCCTAG TGGGGAAGTC
 CTGGTCTCTG TGTACACAG TCACATTTCT TCCGTGGAAG GCCTTACTTT TGAGGGGTCT CTACACGGCC TTTCACATCGT CCACGGGATC ACCCTTTCAG
 104 ThrArgAsp ThrValCysG lncysLysG1 uGlyThrPhe ArgAsnGluA snSerProG1 uMetCysArg LysCysSera rgCysProse rglyGluVal
 601 CAAGTCAGTA ATTGTACGTC CTGGGATGAT ATCCAGTGTG TTGAAGAATT TGGTGCCAAT GCCACTGTGG AAACCCCGAG TGCTGAAGAG ACAATGACCA CCAGCCCGGG
 GTTCAGTCAT TAACATGCAG GACCTACTA TAGGTACAC AACTTCTTAA ACCACGGTTA CCGTGACACC TTTTGGGGTGG ACGACTTCTC TGTTACTTGT
 137 GlnValSera snCysThrse rTrpaspasp lIleGlnCysv alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aAlaGluGlu ThrMetAsnThr
 701 CCAGCCCGGG GACTCTCTGCC CCAGCTGCTG AAGAGACAAT GAACACCAGC CCAGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG
 GGTCCGGGCC CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGTGTGTG CCGTCCCTGAG GACGGGGTGG ACGACTTCTC TGTTACTTGT GGTCCGGGCC
 171 SerProG1 yThrProAla ProAlaAlag luGluThrMe tAsnThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGlyA
 801 GACTCTCTGCC CCAGCTGCTG AAGAGACAAT GACCACCAGC CCGGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCGGG GACTCTCTGCC
 CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGGTGTGTC GGCCTCTGAG GACGGGGTGG ACGACTTCTC TGTTACTTGT GGTCCGGGCC CTGAGGACGG
 204 ThrProAla ProAlaAlag luGluThrMe tThrThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProG1 yThrProAla
 901 TCTTCTCATT ACCTCTCATG CACCATCGTA GGGATCATAG TTTCTAATGT GCTTCTGATT GTGTTTGT TTGAAAGACTTC ACTGTGGAAG AAATTCCTTC
 AGAAGAGTAA TGGAGAGTAC GTGGTAGCAT CCTAGTATC AAGATTAA CA CGAAGACTAA CACAAACAAA CTTTCTGAAG TGACACCTTC TTTAAGGAAG
 237 SerSerHist yrLeuSerCy sThrIleVal GlyIleIlev alLeuIleVal lLeuLeulle ValPheVal
 1001 CTTTACCTGAA AGGTTACAGT AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCCTCC TCTGCTGTGT TCCCACAGAC AGAAACGCCCT
 GAATGGACTT TCCAAGTCCA TCCCGGACCG ACTCCCGCCC CCGCGGACGT GTGAGAGACG GACGGGAGG AGACGACACA AGGTGTCTG TCTTTGCGGA
 1101 GCCCTGCCC CAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA
 CGGGGACGGG GTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

1 GCTGTGGGAA CCTCTCCAG CGACGAACT CAGCCAAAGA TTTCTGATAG ATTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC
CGACACCCCTT GGAGAGGTGC GCGTGTCTGA GTCGGTTGCT AAAGACTATC TAAAAACCTT CAAACTGGTC TCTACGTTCC CCACCTTCTC CGAAGGATG
MetGlnGlu yVallysGlu ArgPh LeuPro

-40

101 CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GCGCGCCTGA TGGCCGAGGC AGGTGCGAC CCAGGACCCA GGACGGCGTC GGAACCATTA CCATGGCCCG
GCAATCCCTT GAGACCCCTG TCTCGCGGCTG CCGCGGACT ACCGGCTCCG TCCACGCTG GGTCTGGGT CCTTGGTAT GGTACCGGGC
-30 L uGlyAs nserGlyAsp ArgAlaProA rgyProProAs pGlyArgGly ArgValArgP roArgThrGl naspglyVal GlyAsnHist hrMetalaArg

201 GATCCCCAAG ACCCTAAAGT TCGTCTCGT CATCTGTCGC GTCTGTCGC CAGTCTTAGC TTTACTCTGCC ACCACTGCCC GGCAGGAGGA AGTTCCCCAG
CTAGGGGTTC TGGGATTCA AGCAGCAGCA GTAGCAGCG CAGGACGACG GTGAGGATCG AATGAGACGG TGGTACCGG CCGTCTCCTT TCAAGGGGTC
4 IleProLys ThrLeuLysP heValValVa lileValAla ValLeuLeuP roValLeuAl aTySerAla ThrThrAlaA rglngluGl uValProGln

301 CAGACAGTGG CCCACAGCA ACAGAGGCAC AGCTTCAAG GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCCGTGCA
GTCTGTACCC GGGGTGTCGT TGTCTCCGTG TCGAAGTTCC CCTCTCTAC AGTCTCTCT AGAGTATCTA GTCTTGTATG ACCTCGGACA TTGGGCACGT
37 GlnThrVala laProGlnG l nGlnArgHis SerPheLysG lyGluGluCy sProAlaGly SerHisArgS erGluHisTh rGlyAlaCys AsnProCysThr

401 CAGAGGGTGT GGATTACACC AACGCTTCCA ACAATGAACC TTCTTGCTTC CCATGTACAG TTGTGTAATC AGATCAAAAA CATAAAAAGTT CTGCACCAT
GTCTCCACA CCTAATGTGG TTGCGAAGGT TGTACTTGG AAGAACGAAG GGTACATGTC AAACATTTAG TCTAGTTTTT GTATTTTCAA GGACGTGGTA
71 GluGlyVa laspTyThr AsnAlaSer a snasngluPr oserCysPhe ProCysThrv alcysLysse rAspGlnLys HisLysSers erCysThrMet

501 GACCAGAGAC ACAGTGTGTC AGTGTAAAGA AGCACCCTTC CGGAATGAAA ACTCCCCAGA GATGTGCGCG AAGTGTAGCA GGTGCCCCTAG TGGGGAAGTC
CTGGTCTCTG TGTACACAG TCACATTTCT TCCGTGAAG GCTTTACTTT TGAGGGTCT CTACACGGCC TTACATCGT CCACGGGATC ACCCTTTCAG
104 ThrArgAsp ThrValCysG lncysLysG l uGlyThrPhe ArgAsnGluA snSerProGl uMetCysArg LysCysSera rgyCysProse rGlyGluVal

601 CAAGTCAGTA ATTGTACGTC CTGGGATGAT ATCCAGTGTG TTGAAGAATT TGGTGCAAT GCACCTGTG AAACCCCGC TGTGTAAGAG ACAATGAACA
GTTTCAGTCAAT TAACATGCAG GACCTACTTA TAGGTACAC AACCTCTTAA ACCACGGTTA CCGTGACACC TTTTGGGGTCG ACGACTTCTC TGTACTTGT
137 GlnValsera snCysThrSe rTrpAspAsp IleGlnCysv alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aAlaGluGlu ThrMetAsnThr

701 CCAGCCCCGG GACTCTCTGCC CCAGCTGCTG AAGAGACAAT GAACACCAGC CCAGGGACTC CTGCCCCAGC TGTGTAAGAG ACAATGACCA CCAGCCCCGG
GGTCGGGGCC CTGAGGACGG GGTGACGGAC TTCTCTGTTA CTGTGCTGTC GTTCTGCTG GGTCCCTGAG GACGGGGTCG ACGACTTCTC TGTACTTGT GGTGCGGCC
171 SerProGl yThrProAla ProAlaAlaG luGluThrMe tAsnThrSer ProGlyThrp roAlaProAl aAlaGluGlu ThrMetThrt hrSerProGly

801 GACTCTCTGC CCAGCTGCTG AAGAGACAAT GACCACCAGC CCGGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA CCAGCCCCGG GACTCTCTGC
CTGAGGACGG GGTGACGAC TTCTCTGTTA CTGTGCTGTC GGTGCTGTC GGTGCTGTC GGTGCTGTC TGTACTTGT GGTGCGGCC CTGAGGACGG
204 ThrProAla ProAlaAlaG luGluThrMe tThrThrSer ProGlyThrp roAlaProAl aAlaGluGlu ThrMetThrt hrSerProGl yThrProAla

901 TCTTCTCATT ACCTCTCATG CACCATCGTA GGGATCATAG TTCTATTTGT GTTTTGTGT GAAAGACTTC ACTGTGGAAG AAATTCCTTC
AGAAAGAGTAA TGGAGAGTAC GTGGTAGCAT CCTAGTATC AAGATTACA CGAAGACTAA CACAAACAAA CTTTCTGAAG TGACACCTTC TTTTAAGGAAG

237 SerSerHist yrLeuSerCy sThrIleVal GlyIleIleVal lLeuLeuIle valPheVal

1001 CTTACTGAA AGGTTACGT AGGCGTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCTCTCC TCTGCTGTGT TCCACAGAC AGAAACGCT
GAATGACTT TCCAAGTCCA TCCGCGACCG ACTCCCGCCC CCGCGGACCT GTGAGAGACG GGCAGGAGG AGACGACACA AGGTGTCTG TCTTTGCGGA

1101 GCCCCTGCC CAAACAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA
CGGGGACGG GTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT

Apo2 1 -----MEQRGQNA~~PAASGARKEHGPGPREAR~~~~C~~RPGLRVPKTLV
 Apo2DcR 1 -----~~MA~~RIPKTLKFVV
 DR4 51 GRGALPTSM~~Q~~GPSAR~~AP~~GRAPGP~~AP~~PAREASPRLLVHKTFKFVVVGVL

Apo2 41 VVAAVLLLVSAESALITQDLA~~Q~~QRAAP~~Q~~QKSSPSEGLCP~~PH~~HISED
 Apo2DcR 13 VIVAVLLPVLAYSATTAR~~Q~~EEV~~Q~~QTVAP~~Q~~Q~~Q~~HSFKGEECPAGSHRSEH
 DR4 101 LQVVPSSAATIK-----LHDSIGTQWEHSPLGELCP~~PG~~SHRSER

Apo2 91 GRDCISCKY~~Q~~QDYSTHW~~N~~DLFC~~R~~CTRED~~S~~GVELSPCTT~~FR~~NTVCOCE
 Apo2DcR 63 TGACNPCTEGVDYTNASN~~NE~~PSCFPCTVCKSDQKHKSCTMT~~RD~~TVCOCK
 DR4 142 PGACNRCTEGVGYNASN~~N~~LFA~~C~~LPCTACKSDEE~~ER~~SPCTT~~FR~~NTACOCK

Apo2 141 EGTFR~~E~~EDSP~~E~~MC~~R~~K~~C~~RTG~~C~~PRG~~M~~V~~K~~VG~~D~~CTP~~W~~SDIECVHKE-----
 Apo2DcR 113 EGTFR~~E~~ENSP~~E~~MC~~R~~K~~C~~SR-CP~~S~~G~~E~~V~~Q~~VS~~N~~CTSW~~D~~DI~~O~~CV~~E~~-EFGANATVE
 DR4 192 PETFR~~N~~DN~~S~~A~~E~~MC~~R~~K~~C~~ST~~E~~C~~P~~R~~G~~M~~V~~K~~V~~K~~D~~CTP~~W~~SDIECVHKE-----

Apo2 -----
 Apo2DcR 161 TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAE
 DR4 -----

Apo2 183 -----SGIIIGVTVA~~AV~~VLIVAVIV---
 Apo2DcR 211 ETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVLIVLLIVFV
 DR4 234 -----SNGHNIWVELV~~VL~~LVPL~~LI~~NAV-LIVC

Apo2 203 EKSLLWKKVL~~P~~YLKGICSGGGGDP~~E~~RVDRSSQRPGAEDNVLNEIVSILQP
 DR4 262 CCIGSGCGGDPKCM~~D~~RVCFWRLGLL~~B~~GPGAEDNAHNEILSNADSLSTFVS

Apo2 253 TQVPEQEMEVOEFAEPTGVNMLSPGESEHLL~~E~~PAEAERSQRRRLIVPANE
 DR4 312 ----EQOMESQEPADLTGVTVQSPGEAQCLLGPAAEGSQRRRLIVPANG

Apo2 303 G~~D~~PTET~~E~~LRQCF~~D~~DFADLVPFDSWEPL~~M~~R~~K~~L~~G~~EMDNEIKVAKAEAA~~G~~H--~~H~~
 DR4 358 ADPTET~~E~~LM~~L~~FFD~~K~~FANIVPFDSWDQ~~L~~MRQ~~L~~DET~~K~~NEIDVVRAGTAGP--~~G~~
 Apo3/DR3 338 VM~~D~~AVPARRWKEFVETLGEREA~~E~~IEAVEVEI-GRF-R
 TNFR1 322 VVENVPPLRWKEFVRR~~L~~GLSDHEIDRL~~E~~LQ~~N~~-GRCLR
 CD95 220 IAGVHTLSQVKG~~F~~VRKNGVNEAKIDEIKNDN-VQDTA

Apo2 351 ~~D~~ILY~~T~~MLIK~~V~~NK~~T~~GR-DASVHTLLDALET~~L~~GERLAKOK~~I~~EDHLLSSGKE
 DR4 406 DALYAM~~L~~M~~K~~V~~N~~K~~T~~GR-NASIH~~T~~LLDALERMEERHAK~~E~~K~~I~~ODLLVDSGKE
 Apo3/DR3 374 DQ~~Q~~YEM~~L~~K~~R~~N~~R~~Q~~Q~~Q~~P~~---AGLGAVYAALERMGLDCVEDLRS
 TNFR1 358 EAQYSMLATWRRR~~E~~PRREATLELLGRVLRDM~~L~~L~~L~~CLEDIEE
 CD95 256 EOKVQLLRNWHQLHGKKEAY-D~~T~~L~~I~~K~~D~~LKKANLCTLAEK~~T~~Q~~T~~

Apo2 400 MYLEG~~N~~ADSALS
 DR4 455 IYLEDGTGSAVSLE

Figure 2

20250103T223010

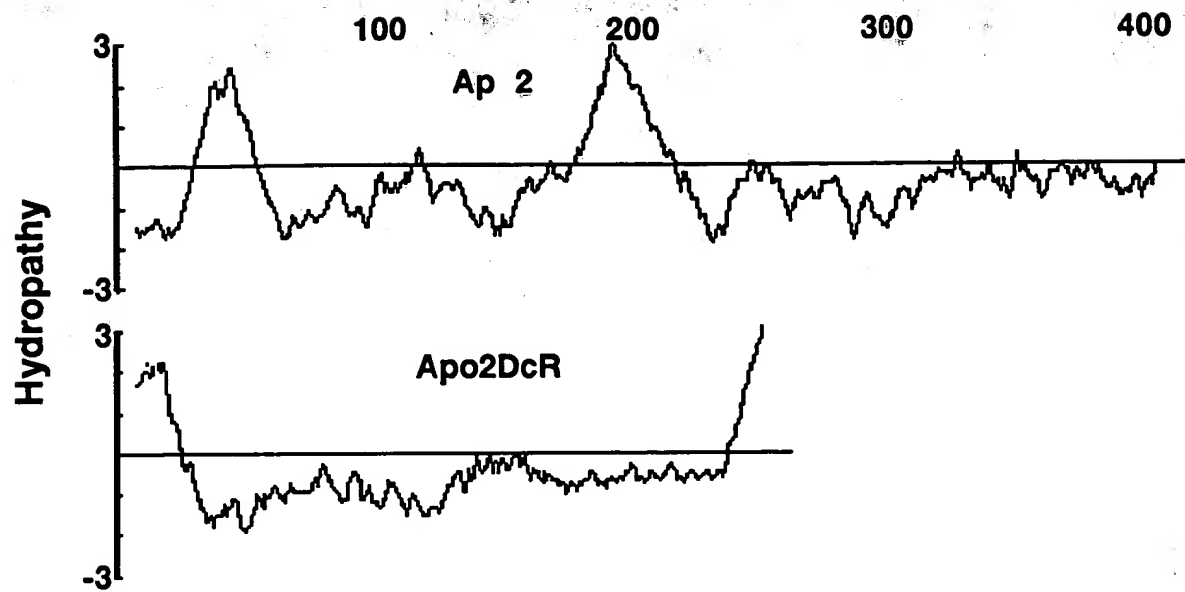


Figure 3

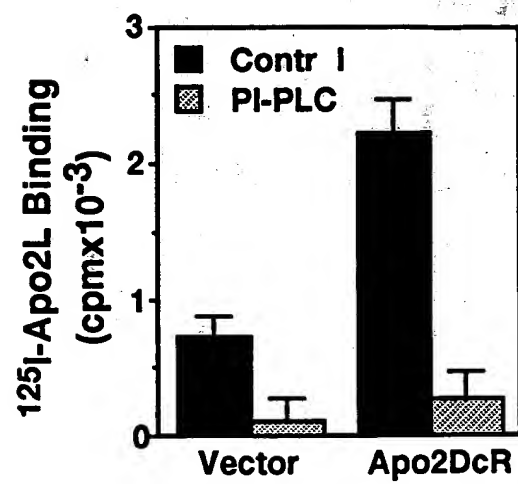


Figure 4

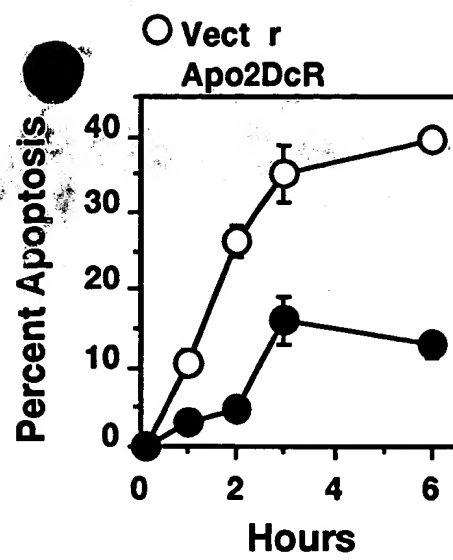


Figure 5

263790783T02B30



Figure 6

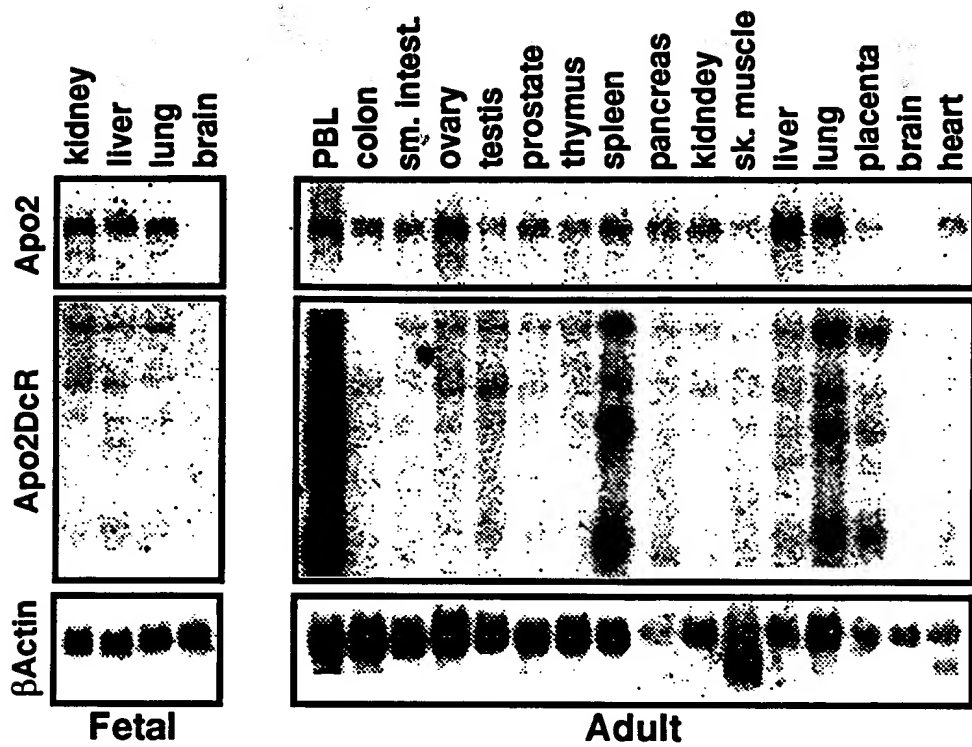


Figure 7

1 CCACGGCGTC GCATRAATC AGCACGGCGC CGGAGAACCC CGCAATCTCT GCGCCACAAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC
GGGTGGCGAG GCGTATTAG TCGTGGCGCG GCCTCTTGGG GCGTTAGAGA CCGGGGTGTT TTATGTGGCT GCTACGGGCT AGATGAAATT CCCGACTTTG
101 CCACGGGCGCT GAGAGACTAT AAGAGCGTTC CCTACCGCCA TGGAAACAAC GGGCCGGCGG CTTCCGGGGC CCGGAAAAGG CACGGGCCAG
GGTGCCCGGA CTCTCTGATA TTCTCGCAAG GGATGGCGGT ACCTTGTTGC CCCTGTCTTG CCGGGCCCGG GAAGCCCCCG GGCCTTTTCC GTCCGGGTG
1 M etGluGlnAr gGlyGlnAsn AlaProAlaA laSerGlyAl aArgLysArg HisGlyProGly
201 GACCCAGGGA GCGCGGGGA GCCAGGCGTG GGCTCGGGT CCCCAGACC CTTGTGCTCG TTGTGCGCGG GGTCTGCTCG TTGGTCTCAG CTGAGTCTGC
CTGGGTCCCT CCGGCCCT CCGTCCGAC CCGAGGCCCA GGGTTCTTG GAACACGAGC AACAGCGCGG CCAGGACGAC AACAGAGTC GACTCAGAGG
22 ProArgG1 uAlaArgGly AlaArgProG lyLeuArgVa lProLysThr LeuValLeuV alValAlaAl aValLeuLeu LeuValSera laGluSerAla
301 TCTGATCAC CAACAAGACC TAGTCCCCA GCAGAGAGCG GCCCAACAAC AAAAGAGGTC CAGCCCCTCA GAGGGATTGT GTCCACCTGG ACACCATATC
AGACTAGTGG GTTGTCTGG ATCGAGGGGT CGTCTCTCGC CCGGTGTTG TTTTCTCCAG GTCGGGGAGT CTCCTTAACA CAGGTGGACC TGTGGTATAG
55 LeuileThr GlnGlnAspL euAlaProG1 nGlnArgAla AlaProGlnG lNlysArgSe rSerProSer GluGlyLeuC ysProProG1 yHisHisile
401 TCAGAAAGAC GTAGAGATTG CATCTCTGC AAATATGGAC AGGACTATAG CACTCAGTGG AATGACCTCC TTTTCTGCTT GCGCTGCACC AGGTGTGATT
AGTCTTCTGC CATCTCTAAC GTAGAGGACG TTTATACCTG TCCTGATATC GTGAGTGACC TTACTGGAGG AAAAGACGAA CCGGACGTGG TCCACACTAA
88 SerGluaspG lyArgaspCy sileSerCys LysTyrglyG lNasPtyrSe rThrHisTrp AsnAspLeuL eupheCysLe uArgCysThr ArgCysaspSer
501 CAGGTGAAGT GGAGCTAAGT CCTGACCA CCAGAGGGAT GGTCAAGGTC GGTGATTGTA CACCCCTGGAG TGACATCGAA AGAATCAGG CATCATCAT
GTCCACTTCA CCTCGATTCA GGCAGTGGT GCTGGTCTTT GTGTACACA GTACACGCTTC TTCCGTGAA GGCCTTCTT CTAAGAGGAC TCTACACGGC
122 GlyGluVa lGluLeuSer ProCysThrT hrThrArgAs hrThrArgAs nThrValCys GlnCysGluG luglyThrph eArgGluGlu AspSerProG luMetCysArg
601 GAAGTCCCGC ACAGGGTGTG CCAGAGGGAT GGTCAAGGTC GGTGATTGTA CACCCCTGGAG TGACATCGAA TGCTGCCACA AAGAATCAGG CATCATCAT
CTTCACGGCG TGTCCACAG GGTCTCCCTA CCAGTTCCAG CCACCTAACAT GTGGGACCTC ACTGTAGCTT ACACAGGTGT TTCTTAGTCC GTAGTAGTAT
155 LysCysArg ThrGlyCysP roArgGlyMe tValLysVal GlyAspCysT hrProTrpSe rAspIleGlu CysValHisL ysGluSerG1 yleIleile
701 GGAGTCACAG TTGCAGCCGT AGTCTTGATT GTGGCTGTGT TTGTTTGCAA GTCTTTACTG TGAAGAAAAG TCCTTCTCTTA CCTGAAAAGG ATCTGCTCAG
CCTCAGTGTG AACGTCGGCA TCAGAACTAA CACCGACACA CACCAACGTT CAGAAATGAC ACCTTCTTTC AGGAAGGAAT GGACTTTCCG TAGACGAGTC
188 GlyValThrV alAlaAlaVa lValleuile ValAlaValP heValCysLy sSerLeuLeu TrpLysLysV alLeuProTy rLeuLysGly ileCysSerGly
801 GTGGTGGTGG GGACCCCTGAG CGTGTGGACA GAAGCTCACA ACCACCTGGG GCTGAGGACA ATGTCTCTCA ATGATCTCTG AGTATCTTGC AGCCACCCCA
CACCACACCC CCTGGGACTC GCACACCTGT CTTCGAGTGT TGCTGGACCC CGACTCCTGT TACAGGAGTT ACTCTAGCAC TCATAGAACG TCGGGTGGGT
222 GlyGlyG1 yaspProGlu ArgValAspa rGserSerG1 narGProGly AlaGluAspa snValLeuAs nGluIleVal serIleLeuG lnProThrGln
901 GGTCCCTGAG CAGGAAATGG AAGTCCAGGA GCCAGCAGAG CCAACAGGTG TCAACATGTT GTCCCCCGGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA
CCAGGGACTC GTCCTTTACC TTCAGGTCTC CCGTGTCTC GGTGTCTCAC AGTTGTACAA CAGGGGGCCC CTCAGTCTCG TAGACGACCT TGGCCGTCTT
255 ValProGlu GlnGluMetG luValGlnG1 uProAlaGlu ProThrGlyV alasnMetLe userProGly GluSerGluH isLeuLeuG1 uProAlaGlu
1001 GCTGAAAGGT CTCAGAGGAG GAGGTGCTG GTTCCAGCAA ATGAAGGTGA TCCCACTGAG ACTCTGAGAC ACTGCTTCCA TGACTTTGCA GACTTTGGTG
CGACTTTCCA GAGTCTCCTC CTCGACGAC CAAGGTGCTT TACTTCCACT AGGTGACTC TGAGACTCTG TCACGAAAGCT ACTGAAACGT CTGAACCCAG
288 AlaGluArgS erGlnArgAr gArgLeuLeu ValProAlaA snGluGlyAs pProThrGlu ThrLeuArgG lnCysPheAs pAspPheAla AspLeuValPro

1101 CCTTTGACTC CTGGGAGCCG CTCATGAGGA AGTTGGGCGCT CATGGACAAAT GAGATTAAGG TGGCTAAAGC TGAGGCAGCG GCCACACAGGG ACACCTTGTA
GGAAACTGAG GACCCCTCGC GAGTACTCCT TCAACCCGGA GTACCTGTTA CTCTATTTC ACCGATTTCG ACTCCGTCGC CCGGTGTCCC TGTGGAACAT
322 PheAspse rTrpGluPro LeuMetArgL ysLeuGlyLe uMetAspAsn GluileLysv alAlaLysAl aGluAlaAla GlyHisArga spThrLeutyx
1201 CACGATGCTG ATAAAGTGGG TCAACAAAAAC CGGGCGAGAT GCCTCTGTCC ACACCTTGCT GAGACGCTGG GAGAGAGACT TGCCAAAGCAG
GTGCTACGAC TATTTCACCC AGTTGTTTTG GCCCGCTCTA CGGAGACAGG TGTGGGACGA CCTACGGAAC CTCTGCGACC CTCTCTCTGA ACGTTTCGTC
355 ThrMetLeu IleLysTrpV alAsnLysTh rGlyArgAsp AlaservAlH isThrLeuLe uAspAlaLeu GluThrLeug lyGluArgLe uAlaLysGln
1301 AAGATTGAGG ACCACTTGTG GAGCTCTGGA AAGTTTCATGT ATCTAGAAGG TAATGCAGAC TCTGCCWTGT CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA
TTCTAACTCC TGGTGAACAA CTCGAGACCT TTCAAGTACA TAGATCTTCC ATTACGTCTG AGACGGAACA GGATTCACAC TAAGAGAAAGT CCTTCACTCT
388 LysIleGluA spHisLeuLe uSerSerGly LysPheMetT yrLeuGluGl yAsnAlaAsp SerAlaXqqS erOC*
1401 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC
GGAAGGGACC AAATGAAAAA AAGACCTTTT TCGGGTTGAC CTGAGGTCAG TCATCCTTTC ACGGTGTAA CAGGTACTG GCCATGACCT TCTTTGAGAG
1501 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT
GGTAGGTTGT AGTGGGTCAC CTACCTTGTA GGACATTGAA AAGTGACGTG AACCGTAATA AAAATATTTCG ACTTACACTA TTATTCTCTGT GATACCTTTA
1601 GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTGTT TGGGATGTCA TTGTTTTTTC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT
CAGACCTAGT AAGGCAACA CGCATGAAAC TCTAAACCAA ACCCTACAGT AACAAAAAGT TCGTGAATAA ATAGGATTAC ATTTACGAAA TAAATAAATA
1701 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAANAAG GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC
AACCAGATGT AACATTCTAG GTAGATGTTT TTTTTTTTTT TTTTTTTTTT CCGCCGGCGC TGAGATCTCA GCTGGACGTC TTCGAACCGG CGGTACCGG

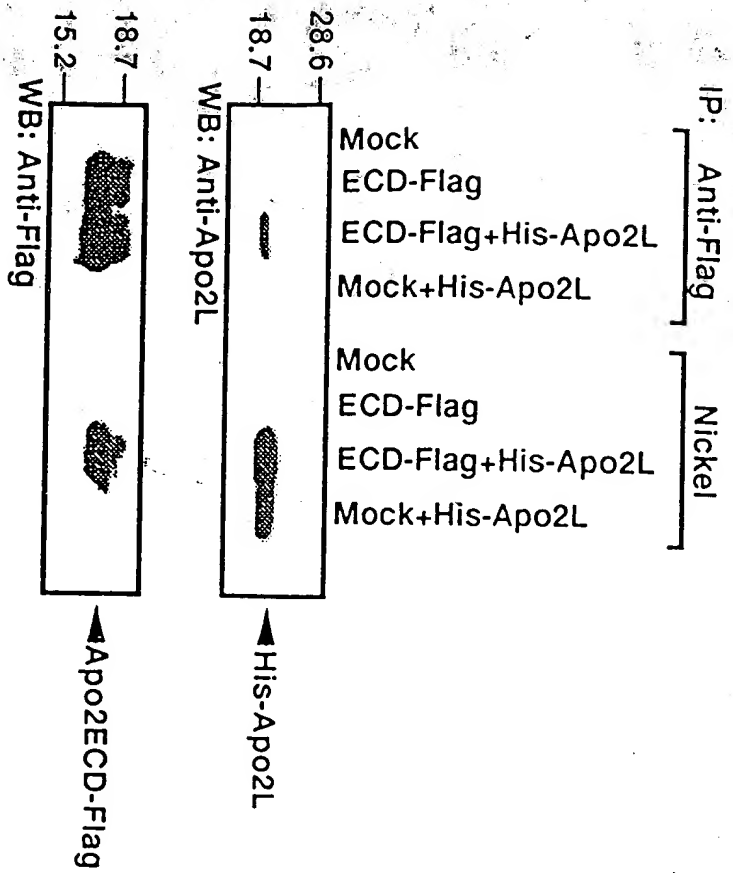
Fig. 8 (cont.)

Fig. 9

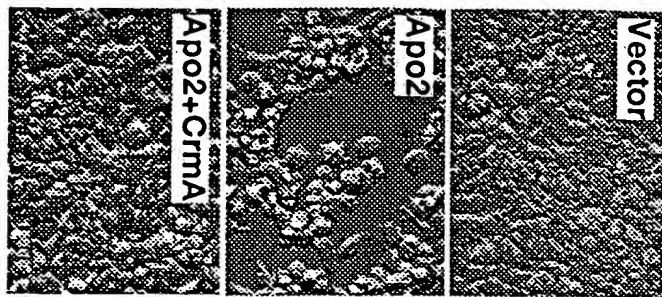
253750-2372430

1 MEORGONAPAAAGARKRHGPGPREARGARPGRLVPKTLVLVAAVLLLVSAESALITQOD
61 LAPQORAAPOQKRSSPSEGLCPPGHHISEDGRDCISQKYQDYSTHWNDDLFLCLRCTRCD
121 SGEVELSPCTTTRNTVCQCEEGTFREEDSPEMCRKCRGTGCPRGMVKVGDC^QTPWSDIECVH
181 KESGIIIGVTVAAVVLIIVAVFVCKSL^WKKVL^WPYLK^WGICSGGGGDPERVDRSSQRP^WGAED
241 NVLNEIVSILQPTQVPEQEMEVEQEP^WAEPTGVNMLSPGESEHLLLEPAEERSQRRRLVPA
301 NEGDPTE^WTLRQC^WFD^WDFADLV^WPFDS^WWEPLMRKIGLMDNEIKVAKAEAAAGHRD^WTL^WTM^WL^WIK^W
361 VNKTGRDASVHTLLDALET^WLG^WER^WLAK^WQ^WK^WIEDHLLSSGKFMYLEGNADSALS

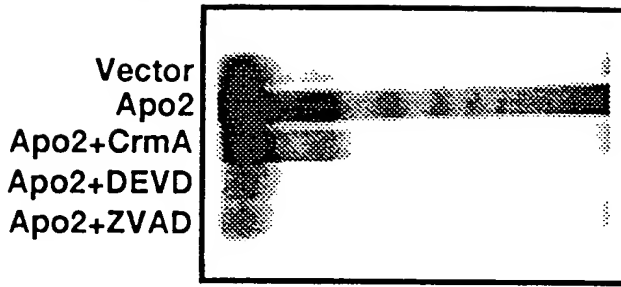
Fig. 10



11A



11B



11C

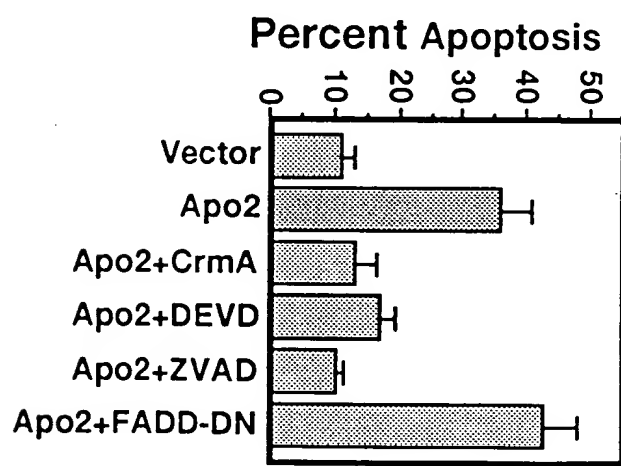
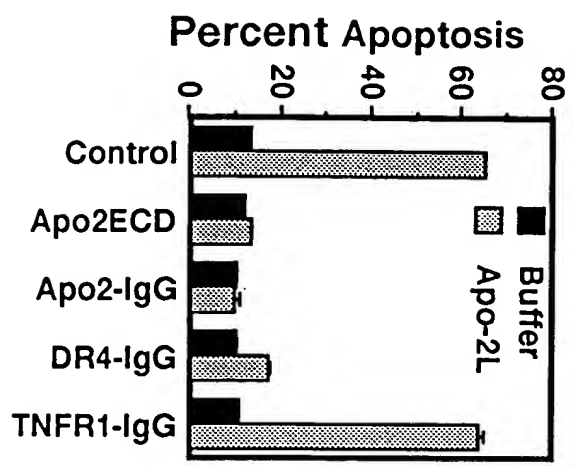
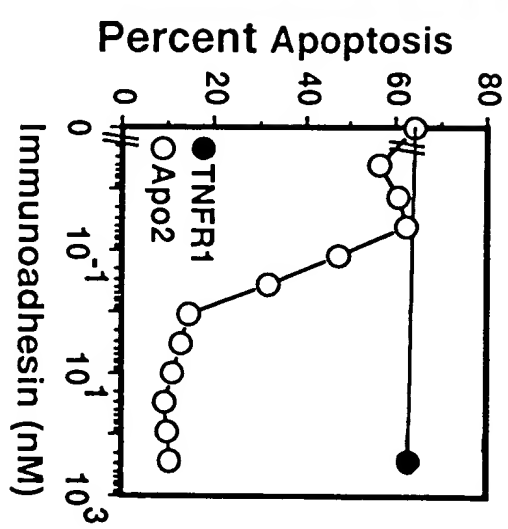


Fig. 11

11D

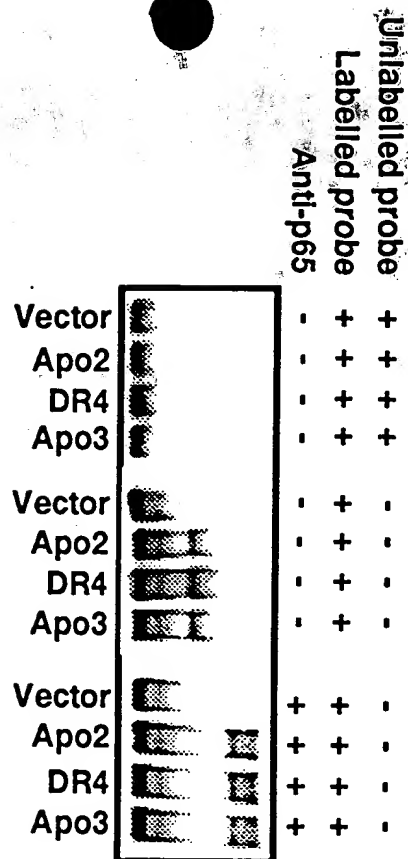


11E

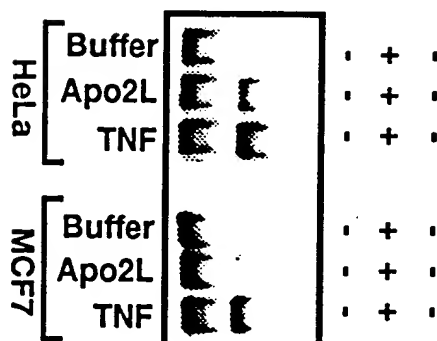


103 101 10-1 10-3

12A



12B



12C

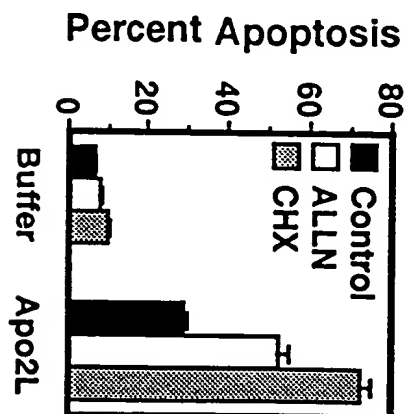


FIG. 12

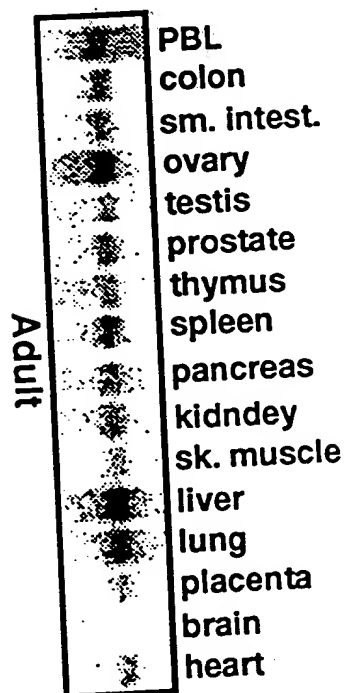
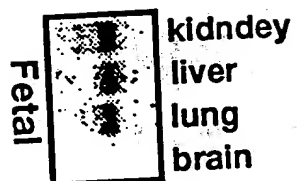


FIG. 13

00072160-061897